

1648
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TECH CENTER 1600/2900



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1600

RAW SEQUENCE LISTING

DATE: 03/27/2002

PATENT APPLICATION: US/09/819,401

TIME: 13:57:52

Input Set : D:\39727-20007.txt

Output Set: N:\CRF3\03272002\I819401.raw

4 <110> APPLICANT: Humeau, Laurent
5 Li, Yuexia
6 Merling, Randal
7 Dropulic, Boro
8 Sconely, Kathy L.
11 <120> TITLE OF INVENTION: CONDITIONALLY REPLICATING VECTORS
12 FOR INHIBITING VIRAL INFECTIONS
15 <130> FILE REFERENCE: 39727-20007.00
17 <140> CURRENT APPLICATION NUMBER: US 09/819,401
18 <141> CURRENT FILING DATE: 2001-03-27
20 <160> NUMBER OF SEQ ID NOS: 18
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 39
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Oligonucleotide encoded wild-type HIV US sequence
32 <400> SEQUENCE: 1
33 gtgtgcccgt ctgttggtgtg actctggttaa ctagagatc 39
35 <210> SEQ ID NO: 2
36 <211> LENGTH: 39
37 <212> TYPE: DNA
38 <213> ORGANISM: Artificial Sequence
40 <220> FEATURE:
41 <223> OTHER INFORMATION: Vector sequence
43 <400> SEQUENCE: 2
44 gtgtgcccac ctgttggtgtg actctggcag ctagagaac 39
46 <210> SEQ ID NO: 3
47 <211> LENGTH: 40
48 <212> TYPE: DNA
49 <213> ORGANISM: Artificial Sequence
51 <220> FEATURE:
52 <223> OTHER INFORMATION: Sequence encoded ribozyme
54 <400> SEQUENCE: 3
55 cacacaacac tgatgaggcc gaaaggccga aacgggcaca 40
57 <210> SEQ ID NO: 4
58 <211> LENGTH: 40
59 <212> TYPE: DNA
60 <213> ORGANISM: Artificial Sequence
62 <220> FEATURE:
63 <223> OTHER INFORMATION: Sequence encoded ribozyme
65 <400> SEQUENCE: 4

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66 atctctagtc tgatgaggcc gaaaggccga aaccagagtc          40
68 <210> SEQ ID NO: 5
69 <211> LENGTH: 39
70 <212> TYPE: DNA
71 <213> ORGANISM: Artificial Sequence
73 <220> FEATURE:
74 <223> OTHER INFORMATION: Vector sequence
76 <400> SEQUENCE: 5
77 gtgtgcccgc ctgttggtgtg actctggtaa ctagagatc          39
79 <210> SEQ ID NO: 6
80 <211> LENGTH: 39
81 <212> TYPE: DNA
82 <213> ORGANISM: Artificial Sequence
84 <220> FEATURE:
85 <223> OTHER INFORMATION: Vector sequence
87 <400> SEQUENCE: 6
88 gtgtgcccgt ctgttggtgtg actctggcaa ctagagatc          39
90 <210> SEQ ID NO: 7
91 <211> LENGTH: 15
92 <212> TYPE: DNA
93 <213> ORGANISM: Artificial Sequence
95 <220> FEATURE:
96 <223> OTHER INFORMATION: Consensus splice donor
98 <221> NAME/KEY: misc_feature
99 <222> LOCATION: (1)...(15)
100 <223> OTHER INFORMATION: n = A,T,C or G
102 <400> SEQUENCE: 7
W--> 103 nnnnaggtaa gtann          15
105 <210> SEQ ID NO: 8
106 <211> LENGTH: 15
107 <212> TYPE: DNA
108 <213> ORGANISM: Artificial Sequence
110 <220> FEATURE:
111 <223> OTHER INFORMATION: Beta-globin splice donor
113 <221> NAME/KEY: misc_feature
114 <222> LOCATION: (1)...(15)
115 <223> OTHER INFORMATION: n = A,T,C or G
117 <400> SEQUENCE: 8
W--> 118 ngggcaggta agtat          15
120 <210> SEQ ID NO: 9
121 <211> LENGTH: 15
122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: HIV major splice donor
128 <221> NAME/KEY: misc_feature
129 <222> LOCATION: (1)...(15)
130 <223> OTHER INFORMATION: n = A,T,C or G
132 <400> SEQUENCE: 9

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W--> 133 nngactggtg agtan 15
135 <210> SEQ ID NO: 10
136 <211> LENGTH: 15
137 <212> TYPE: DNA
138 <213> ORGANISM: Artificial Sequence
140 <220> FEATURE:
141 <223> OTHER INFORMATION: HIV-1 env splice donor
143 <400> SEQUENCE: 10
144 aaagcagtaa gtagt 15
146 <210> SEQ ID NO: 11
147 <211> LENGTH: 15
148 <212> TYPE: DNA
149 <213> ORGANISM: Artificial Sequence
151 <220> FEATURE:
152 <223> OTHER INFORMATION: HIV-2 env splice donor
154 <400> SEQUENCE: 11
155 agacaagtga gtaag 15
157 <210> SEQ ID NO: 12
158 <211> LENGTH: 15
159 <212> TYPE: DNA
160 <213> ORGANISM: Artificial Sequence
162 <220> FEATURE:
163 <223> OTHER INFORMATION: HIV-2 major splice donor
165 <221> NAME/KEY: misc_feature
166 <222> LOCATION: (1)...(15)
167 <223> OTHER INFORMATION: n = A,T,C or G
169 <400> SEQUENCE: 12
W--> 170 nngaaggtaa gtgcn 15
172 <210> SEQ ID NO: 13
173 <211> LENGTH: 112
174 <212> TYPE: DNA
175 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Double-stranded oligonucleotide
180 <400> SEQUENCE: 13
181 aagcttgccct tgagtgtca aagtagtgtg tgccacctg ttgtgtgact ctggcagcta 60
182 gagatccac agaccctttt agtcagtgtg gaaaatctct agcagtggcg cc 112
184 <210> SEQ ID NO: 14
185 <211> LENGTH: 39
186 <212> TYPE: DNA
187 <213> ORGANISM: Artificial Sequence
189 <220> FEATURE:
190 <223> OTHER INFORMATION: Oligonucleotide with mutant nucleotides
192 <221> NAME/KEY: misc_feature
193 <222> LOCATION: (1)...(39)
194 <223> OTHER INFORMATION: n = A,T,C or G
196 <400> SEQUENCE: 14
W--> 197 gtgtgcccn ctgttgtgtg actctggnan ctagaganc 39
199 <210> SEQ ID NO: 15

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200 <211> LENGTH: 39
201 <212> TYPE: DNA
202 <213> ORGANISM: Artificial Sequence
204 <220> FEATURE:
205 <223> OTHER INFORMATION: Mutated oligonucleotide
207 <400> SEQUENCE: 15
208 gtgtgccccat ctgttggtgtg actctggtaa ctagagatc      39
210 <210> SEQ ID NO: 16
211 <211> LENGTH: 39
212 <212> TYPE: DNA
213 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: Mutated oligonucleotide
218 <400> SEQUENCE: 16
219 gtgtgcccgt ctgttggtgtg actctggtag ctagagatc      39
221 <210> SEQ ID NO: 17
222 <211> LENGTH: 16
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: Analog splice donor
229 <221> NAME/KEY: misc_feature
230 <222> LOCATION: (1)...(16)
231 <223> OTHER INFORMATION: n = A,T,C or G
233 <400> SEQUENCE: 17
W--> 234 cttcaggggtg agttnn      16
236 <210> SEQ ID NO: 18
237 <211> LENGTH: 1185
238 <212> TYPE: PRT
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
242 <223> OTHER INFORMATION: Amino acid sequence of a chimeric HIV CTL epitope
244 <400> SEQUENCE: 18
245 Met Lys Ile Arg Leu Arg Pro Gly Gly Asn Lys Lys Tyr Lys Leu Lys
246 1          5          10          15
247 His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Gly Ser Glu Glu
248          20          25          30
249 Leu Arg Ser Leu Tyr Asn Thr Val Ala Val Leu Tyr Cys Val His Gln
250          35          40          45
251 Lys Ile Glu Val Lys Asp Thr Lys Glu Ala Leu Asp Thr Glu Asn Arg
252          50          55          60
253 Asn Gln Glu Ser Gln Asn Tyr Pro Ile Val Gln Asn Leu Gly Gln Met
254 65          70          75          80
255 Val His Gln Ala Leu Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val
256          85          90          95
257 Ile Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala
258          100         105         110
259 Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr
260          115         120         125

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```

261 Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Ala Thr Ile Asn
262      130      135      140
263 Glu Glu Ala Ala Glu Trp Asp Arg Leu His Pro Val His Ala Gly Pro
264 145      150      155      160
265 Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Thr Ser Thr Leu Gln
266      165      170      175
267 Glu Gln Ile Ala Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly Glu
268      180      185      190
269 Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg Met
270      195      200      205
271 Tyr Ser Pro Val Ser Ile Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys
272      210      215      220
273 Thr Leu Arg Ala Glu Gln Ala Thr Gln Glu Val Lys Asn Trp Met Thr
274 225      230      235      240
275 Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu
276      245      250      255
277 Lys Ala Leu Leu Glu Asp Met Met Thr Ala Cys Gln Gly Val Gly Gly
278      260      265      270
279 Pro Gly His Lys Ala Arg Leu Val Gln Glu Gly His Gln Met Lys Asp
280      275      280      285
281 Cys Thr Glu Arg Gln Ala Asn Phe Gly Asn Phe Pro Gln Ser Arg Leu
282      290      295      300
283 Glu Pro Thr Ala Pro Pro Glu Ile Thr Leu Trp Gln Arg Pro Leu Val
284 305      310      315      320
285 Asp Thr Val Leu Glu Asp Met Asn Leu Val Leu Val Gly Pro Thr Pro
286      325      330      335
287 Val Asn Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Gly Pro Lys
288      340      345      350
289 Val Lys Gln Trp Pro Leu Ala Leu Val Glu Ile Cys Thr Glu Met Glu
290      355      360      365
291 Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Thr Val Leu Asp Val Gly
292      370      375      380
293 Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr
294 385      390      395      400
295 Ala Phe Thr Ile Pro Ser Ile Trp Lys Gly Ser Pro Ala Ile Phe Gln
296      405      410      415
297 Ser Ser Met Thr Lys Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp
298      420      425      430
299 Asp Leu Tyr Val Asp Leu Glu Glu Gly Gln His Arg Thr Lys Ile Glu
300      435      440      445
301 Glu Leu Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys
302      450      455      460
303 Lys Pro Ile Lys Leu Pro Glu Lys Glu Ser Trp Leu Val Gly Lys Leu
304 465      470      475      480
305 Asn Trp Ala Ser Gln Ile Tyr Ala Gly Ile Lys Val Lys Gln Leu Ile
306      485      490      495
307 Pro Ile Thr Glu Glu Ala Glu Leu Glu Ile Leu Lys Glu Pro Val His
308      500      505      510
309 Gly Val Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly

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VERIFICATION SUMMARY

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Input Set : D:\39727-20007.txt

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L:103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:118 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:197 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17